

IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/791,619

DATE: 08/30/2004 TIME: 14:48:42

Input Set : N:\Crf3\RULE60\10791619.raw.txt
Output Set: N:\CRF4\08302004\J791619.raw

```
1 <110> APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe 2 <120> TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving olypeptides

3 <130> FILE REFERENCE: P1123R1

4 <140> CURRENT APPLICATION NUMBER: US/10/791,619

5 <141> CURRENT FILING DATE: 2004-03-02

6 <150> PRIOR APPLICATION NUMBER: US/09/109,207

7 <151> PRIOR FILING DATE: 1998-06-30

8 <150> PRIOR APPLICATION NUMBER: US 60/051,554

9 <151> PRIOR FILING DATE: 1997-07-03

10 <160> NUMBER OF SEQ ID NOS: 44

12 <210> SEQ ID NO: 1

13 <211> LENGTH: 6127

14 <212> TYPE: DNA
```

15 <213> ORGANISM: Artificial

16 <220> FEATURE:

29

30 31

32

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34

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36 37

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39

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41

42

43

cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag agcttcaaca 1150

ggggagagtg ttaagctgat cetetaegee ggacgeateg tggeeetagt 1200

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45 acgcaagttc acgtaaaaag ggtatctaga ggttgaggtg attttatgaa 1250 46 aaagaatatc gcatttcttc ttgcatctat gttcgttttt tctattgcta 1300 47 caaacgcgta cgctgaggtt cagctggtgg agtctggcgg tggcctggtg 1350 48 cagccagggg getcactccg tttgtcctgt gcagtttctg getactccat 1400 49 cacctccgga tacagctgga actggatccg tcaggccccg ggtaagggcc 1450 50 tggaatgggt tgcatcgatt acgtatgacg gatcgactaa ctataaccct 1500 agegteaagg geegtateae tataagtege gaegatteea aaaacacatt 1550 51 52 ctacctgcag atgaacagcc tgcgtgctga ggacactgcc gtctattatt 1600 53 gtgctcgagg cagccactat ttcggtcact ggcacttcgc cgtgtggggt 1650 54 caaggaaccc tggtcaccgt ctcctcggcc tccaccaagg gcccatcggt 1700 55 cttcccccta gcaccctcct ccaagagcac ctctgggggc acagcggccc 1750 56 tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1800 57 aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca 1850 58 gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg ccctccagca 1900 59 gettgggeac ceagacetac atetgeaacg tgaateacaa geecageaac 1950 60 accaaqqtqq acaaqaaaqt tqaqcccaaa tcttqtqaca aaactcacac 2000 61 ctagagtggc ggtggctctg gttccggtga ttttgattat gaaaagatgg 2050 62 caaacgctaa taagggggct atgaccgaaa atgccgatga aaacgcgcta 2100 63 cagtctgacg ctaaaggcaa acttgattct gtcgctactg attacggtgc 2150 64 tgctatcgat ggtttcattg gtgacgtttc cggccttgct aatggtaatg 2200 65 qtgctactgg tgattttgct ggctctaatt cccaaatggc tcaagtcggt 2250 66 gacggtgata attcaccttt aatgaataat ttccgtcaat atttaccttc 2300 67 ceteceteaa teggttgaat gtegeeettt tgtetttage getggtaaac 2350 68 catatgaatt ttctattgat tgtgacaaaa taaacttatt ccgtggtgtc 2400 69 tttgcgtttc ttttatatgt tgccaccttt atgtatgtat tttctacgtt 2450 70 tgctaacata ctgcgtaata aggagtctta atcatgccag ttcttttggc 2500 71 tagegeegee ctatacettg tetgeeteee egegttgegt egeggtgeat 2550 72 ggagceggge caectegace tgaatggaag eeggeggeac etegetaaeg 2600 73 gattcaccac tccaagaatt ggagccaatc aattcttgcg gagaactgtg 2650 74 aatgcgcaaa ccaacccttg gcagaacata tccatcgcgt ccgccatctc 2700 75 cagcageege acgeggegea tetegggeag egttgggtee tggccaeggg 2750 76 tgcgcatgat cgtgctcctg tcgttgagga cccggctagg ctggcggggt 2800 77 tgccttactg gttagcagaa tgaatcaccg atacgcgagc gaacgtgaag 2850 78 cgactgctgc tgcaaaacgt ctgcgacctg agcaacaaca tgaatggtct 2900 79 teggttteeg tgtttegtaa agtetggaaa egeggaagte agegeeetge 2950 80 accattatgt teeggatetg categoagga tgetgetgge taccetgtgg 3000 81 aacacctaca tetgtattaa egaagegetg geattgacce tgagtgattt 3050 82 ttetetggte eegeegeate catacegeea gttgtttace etcacaaegt 3100 83 tecagtaace gggeatgtte atcateagta acceptateg tgageatect 3150 84 ctctcgtttc atcggtatca ttacccccat gaacagaaat tcccccttac 3200 85 acggaggcat caagtgacca aacaggaaaa aaccgccctt aacatggccc 3250 86 getttateag aagecagaca ttaaegette tggagaaact caaegagetg 3300 87 gacgcggatg aacaggcaga catctgtgaa tcgcttcacg accacgctga 3350 88 tgagetttae egeaggatee ggaaattgta aaegttaata ttttgttaaa 3400 89 attegegtta aattittigtt aaateagete attitttaac caataggeeg 3450 90 aaatcggcaa aatcccttat aaatcaaaag aatagaccga gatagggttg 3500 91 agtgttgttc cagtttggaa caagagtcca ctattaaaga acgtggactc 3550 92 caacgtcaaa gggcgaaaaa ccgtctatca gggctatggc ccactacgtg 3600 93

aaccatcacc ctaatcaagt tttttggggt cgaggtgccg taaagcacta 3650

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Input Set: N:\Crf3\RULE60\10791619.raw.txt
Output Set: N:\CRF4\08302004\J791619.raw

| 94 | | | | | ggggaaagcc | |
|-----|--------------|------------|--------------|--------------|--------------|------|
| 95 | | | | | gcgggcgcta | |
| 96 | | | | | cacacccgcc | |
| 97 | gcgcttaatg | cgccgctaca | gggcgcgtcc | ggatcctgcc | tcgcgcgttt | 3850 |
| 98 | cggtgatgac | ggtgaaaacc | tctgacacat | gcagctcccg | gagacggtca | 3900 |
| 99 | cagcttgtct | gtaagcggat | gccgggagca | gacaagcccg | tcagggcgcg | 3950 |
| 100 | tcagcgggtg | ttggcgggtg | ı teggggegea | gccatgaccc | agtcacgtag | 4000 |
| 101 | cgatagcgga | gtgtatactg | gcttaactat | geggeateag | , agcagattgt | 4050 |
| 102 | actgagagtg | caccatatgo | ggtgtgaaat | . accgcacaga | ı tgcgtaagga | 4100 |
| 103 | | | | | tgactcgctg | |
| 104 | | | | | caaaggcggt | |
| 105 | | | | | , aacatgtgag | |
| 106 | | | | | gttgctggcg | |
| 107 | | | | | atcgacgctc | |
| 108 | | | | | caggcgtttc | |
| 109 | | | | | gccgcttacc | |
| 110 | | | | | tttctcatag | |
| 111 | | | | | tccaagctgg: | |
| 112 | | | | | cttatccggt | |
| 113 | | | | | cgccactggc | |
| 114 | | | | | ggcggtgcta | |
| 115 | | | | | g aaggacagta | |
| 116 | | | | | aaagagttgg | |
| 117 | | | | | ggttttttg | |
| 118 | | | | | agaagatcct | |
| 119 | | | | | actcacgtta | |
| 120 | | | | | tagatccttt | |
| 121 | | | | | tgagtaaact | |
| 122 | | | | | tctcagcgat | |
| 123 | | | | | gtgtagataa | |
| 124 | | | | | aatgataccg | |
| 125 | | | | | | |
| 126 | | | | | accagccagc | |
| 127 | | | | | gcctccatcc | |
| | | | | | gccagttaat | |
| 128 | | | | | tgtcacgctc | |
| 129 | | | | | tcaaggcgag | |
| 130 | | | | | cttcggtcct | |
| 131 | | | | | tcatggttat | |
| 132 | | | | | agatgctttt | |
| 133 | | | | | gtgtatgcgg | |
| 134 | | | | | ccgcgccaca | |
| 135 | | | | | tcggggcgaa | |
| 136 | - | | | _ | gtaacccact | |
| 137 | | - | - | | gcgtttctgg | |
| 138 | | | | | ataagggcga | |
| 139 | | | | | ttattgaagc | |
| 140 | | | | | , aatgtattta | |
| 141 | | | | | aaagtgccac | |
| 142 | ctgacgtcta | agaaaccatt | attatcatga | a cattaaccta | ı taaaaatagg | 6100 |
| | | | | | | |

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```
cgtatcacga ggccctttcg tcttcaa 6127
  143
  145 <210> SEQ ID NO: 2
  146 <211> LENGTH: 121
  147 <212> TYPE: PRT
  148 <213> ORGANISM: Mus musculus
  149 <400> SEQUENCE: 2
             Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
  150
  151
             Gln Ser Leu Ser Leu Ala Cys Ser Val Thr Gly Tyr Ser Ile Thr
  152
                               20
                                                    25
  153
             Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys
  154
  155
             Leu Glu Trp Met Gly Ser Ile Thr Tyr Asp Gly Ser Ser Asn Tyr
  156
  157
                               50
             Asn Pro Ser Leu Lys Asn Arg Ile Ser Val Thr Arg Asp Thr Ser
  158
                               65
  159
             Gln Asn Gln Phe Phe Leu Lys Leu Asn Ser Ala Thr Ala Glu Asp
  160
                                                                         90
                               80
                                                    85
  161
             Thr Ala Thr Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
  162
                                                   100
                               95
  163
             Trp His Phe Ala Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser
  164
                                                   115
                              110
  165
             Ser
  166
  168 <210> SEQ ID NO: 3
  169 <211> LENGTH: 121
  170 <212> TYPE: PRT
  171 <213> ORGANISM: Artificial
  172 <220> FEATURE:
\sim 173 <221> NAME/KEY: Artificial
  174 <222> LOCATION: 1-121
  175 <223> OTHER INFORMATION: F(ab) sequence derived from MAE11
  176 <400> SEOUENCE: 3
             Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
  177
  178
             Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile Thr
  179
                               20
                                                    25
  180
             Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly
  181
                                                    40
  182
                               35
             Leu Glu Trp Val Ala Ser Ile Thr Tyr Asp Gly Ser Thr Asn Tyr
  183
                                                                         60
                                                    55
  184
             Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
  185
                              65
                                                    70
  186
             Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
  187
                                                    85
  188
             Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
  189
                                                   100
                               95
  190
             Trp His Phe Ala Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
  191
                                                   115
                                                                        120
                              110
  192
  193
              Ser
```

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Output Set: N:\CRF4\08302004\J791619.raw

```
196 <211> LENGTH: 121
     197 <212> TYPE: PRT
     198 <213> ORGANISM: Homo sapiens
     199 <220> FEATURE:
     200 <221> NAME/KEY: unsure
     201 <222> LOCATION: 30, 104-108
     202 <223> OTHER INFORMATION: unknown amino acid
     203 <400> SEQUENCE: 4
                Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
     204
     205
                Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa
W --> 206
     207
                Ser Asp Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
     208
     209
                Leu Glu Trp Val Ala Val Ile Ser Asn Gly Ser Asp Thr Tyr Tyr
     210
                                                                            60
     211
                Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
     212
     213
                                  65
                                                       70
     214
                Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
     215
                                  80
                                                       85
   > 216
                Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Arg Phe Phe Xaa Xaa
     217
                                  95
                                                      100
   > 218
                Xaa Xaa Xaa Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
     219
                                 110
                                                      115
                                                                           120
     220
                Ser
     222 <210> SEQ ID NO: 5
     223 <211> LENGTH: 111
     224 <212> TYPE: PRT
     225 <213> ORGANISM: Mus musculus
     226 <400> SEQUENCE: 5
                Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu
     227
     228
     229
                Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp
                                                                            30
     230
                                  20
                Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
     231
     232
                Gln Pro Pro Ile Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Gly Ser
     233
     234
                                  50
                                                       55
                Glu Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
     235
     236
                Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Phe
     237
                                  80 .
     238
                                                       85
                Tyr Cys Gln Gln Ser His Glu Asp Pro Tyr Thr Phe Gly Ala Gly
     239
                                                      100
     240
     241
                Thr Lys Leu Glu Ile Lys
     242
                                 110
     244 <210> SEQ ID NO: 6
     245 <211> LENGTH: 111
```

195 <210> SEQ ID NO: 4

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/791,619

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Input Set : N:\Crf3\RULE60\10791619.raw.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:7; Xaa Pos. 33,34

Seq#:36; N Pos. 16,17,19,20,25,26,28,29

Seq#:37; N Pos. 16,17,19,20,22,28,29

Seq#:38; N Pos. 16,17,19,20,22,23,28,29,34,35

Seq#:39; N Pos. 17,18,20,21,23,24,26,27

Seq#:40; N Pos. 21,22,24,25,27,28,33,34

Seq#:41; N Pos. 17,18,20,21,23,24,26,27,29,30

Seq#:42; N Pos. 22,23,25,26,28,29,34,35

Seq#:43; N Pos. 15,16,18,19,21,22,27,28,33,34

Seq#:44; N Pos. 16,17,19,20,25,26,31,32
```

Seq#:4; Xaa Pos. 30,104,105,106,107,108

Invalid Line Length:

Seq#:1; Line(s) 1,2

The rules require that a line not exceed 72 characters in length. This includes spaces.

```
Seq#:36; Line(s) 1201
Seq#:37; Line(s) 1215
Seq#:38; Line(s) 1229
Seq#:39; Line(s) 1243
Seq#:40; Line(s) 1257
Seq#:41; Line(s) 1272
Seq#:42; Line(s) 1286
Seq#:43; Line(s) 1301
Seq#:44; Line(s) 1316
```

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,3,6,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30 Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/791,619 TIME: 14:48:43

DATE: 08/30/2004

Input Set : N:\Crf3\RULE60\10791619.raw.txt
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```
L:17 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:15
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:90
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:105
L:249 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:30
L:301 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:327 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:353 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:379 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:405 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:431 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:471 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:542 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:582 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:653 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:693 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:764 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:804 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:845 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:886 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:930 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:974 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:1014 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:1056 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1098 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:1109 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:1120 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:1131 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:1142 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:1154 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:1165 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:1176 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:1188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:1199 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:1205 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1213 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:1219 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1227 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:1233 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:38
L:1234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:1241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:1247 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:39
L:1248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:1255 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
```

VERIFICATION SUMMARY

L:1321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0

DATE: 08/30/2004 TIME: 14:48:43

PATENT APPLICATION: US/10/791,619 TI

Input Set: N:\Crf3\RULE60\10791619.raw.txt
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L:1261 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:40
L:1262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:1270 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:1276 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41
L:1277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1284 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42
L:1290 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:1291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:1299 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1305 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:1314 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
L:1320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:44